AMENDMENTS TO THE CLAIMS

Claims 1 to 28 (Cancelled)

29. (New) A method of diagnosing Alzheimer's disease comprising:

a) determining the expression level of a polypeptide of SEQ ID NO:2 or a fragment thereof in a normal brain sample and a brain test sample; and

b) comparing said expression level of said polypeptide from said brain test sample with said expression level of said polypeptide from said brain test sample; wherein an elevated expression level of said polypeptide in said test sample relative to the expression level of said polypeptide in said normal sample is indicative of Alzheimer's disease or a predisposition to Alzheimer's disease.

30. (New) The method according to Claim 29, wherein said expression level is determined by measuring the transcript level of RNA encoding said polypeptide.

31. (New) The method according to Claim 29, wherein said expression level is determined by protein measurement.

32. (New) The method according to Claim 30, wherein said RNA measurement comprises specific hybridization between said RNA to a member of the group consisting of:

a) an isolated nucleic acid comprising SEQ ID NO:1;

b) an isolated nucleic acid comprising nucleotides 4 to 1020 of SEQ ID NO:1;

c) an isolated nucleic acid comprising nucleotides 1 to 1020 of SEQ ID NO:1;

d) an isolated nucleic acid comprising the HGPRBMY9 cDNA clone contained in ATCC Deposit No. PTA-2675; and

e) an isolated nucleic acid comprising the complementary sequence of (a), (b), (c), or (d).

33. (New) The method according to Claim 31, wherein said RNA measurement comprises specific hybridization between said RNA to an isolated nucleic acid comprising at least 12 contiguous nucleotides of nucleotides 4 to 1020 of SEQ ID NO:1, or complete complement thereof.

34. (New) The method according to Claim 33, wherein said RNA measurement further comprises a second isolated nucleic acid comprising at least 12 contiguous nucleotides of nucleotides 4 to 1020 of SEQ ID NO:1, or complete complement thereof, wherein said isolated nucleic acid is directed to the sense strand, and said second isolated nucleic acid is directed to the antisense strand, wherein said hybridization is followed by at least one amplification step.

35. (New) The method according to Claim 31, wherein said protein measurement comprises detecting a member of the group consisting of:

a.) an isolated polypeptide comprising SEQ ID NO:2;
b.) an isolated polypeptide comprising amino acids 1 to 340 of SEQ ID NO:2;
c.) an isolated polypeptide comprising amino acids 2 to 340 of SEQ ID NO:2; and
d.) an isolated polypeptide consisting of the polypeptide encoded by the HGPRBMY9 cDNA clone contained in ATCC Deposit No. PTA-2675.

36. (New) The method according to Claim 35, wherein said protein measurement utilizes an antibody that specifically binds to said member.

37. (New) The method according to Claim 31, wherein said protein measurement comprises detecting an isolated polypeptide comprising at least 7 contiguous amino acids of SEQ ID NO:2.

38. (New) The method according to Claim 37, wherein said protein measurement utilizes an antibody that specifically binds to said contiguous amino acid.